

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: May 18, 2002, 02:09:56 ; Search time 8718.72 Seconds  
(without alignments)  
1893.746 Million cell updates/sec

Title: US-09-719-748-1\_COPY\_98\_886

Perfect score: 789  
Sequence: 1 tatgacatcgagagagagct.....ctctcagacaccctggtac 789

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl: \*  
1: gb\_ba: \*  
2: gb\_hlg: \*  
3: gb\_in: \*  
4: gb\_om: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_pl: \*  
9: gb\_pr: \*  
10: gb\_ro: \*  
11: gb\_sts: \*  
12: gb\_sy: \*  
13: gb\_un: \*  
14: gb\_vl: \*  
15: em\_ba: \*  
16: em\_fun: \*  
17: em\_hum: \*  
18: em\_in: \*  
19: em\_mu: \*  
20: em\_om: \*  
21: em\_or: \*  
22: em\_ov: \*  
23: em\_pat: \*  
24: em\_ph: \*  
25: em\_pl: \*  
26: em\_ro: \*  
27: em\_sts: \*  
28: em\_un: \*  
29: em\_vl: \*  
30: em\_hlg\_hum: \*  
31: em\_hlg\_inv: \*  
32: em\_hlg\_other: \*  
33: em\_hlgo\_inv: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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1	787.4	99.8	1742	9	AF052941 Homo sapi
2	784.2	99.4	1739	9	AB018001 Homo sapi
3	697.8	88.4	1883	10	BC022165 Mus muscu
4	693	87.8	1757	10	AB018002 Mus muscu
5	569.6	72.2	1474	10	AF052942 Mus muscu
6	495.2	62.8	2055	9	AB022341 Homo sapi
7	494.6	62.7	1410	10	AB007143 Mus muscu
8	494.6	62.7	1429	6	AB076190 Sequence
9	494.6	62.7	1429	6	AR124103 Sequence
10	494.6	62.7	1429	6	E23385 DNA encodin
11	493.6	62.6	2105	9	AB007144 Homo sapi
12	493.6	62.6	2132	6	AR076189 Sequence
13	493.6	62.6	2132	6	AR124102 Sequence
14	493.6	62.6	2132	6	E23384 DNA encodin
15	493.6	62.6	2224	6	BD004888 Novel gen
16	493.6	62.6	2224	9	AK027590 Homo sapi
17	480.2	60.9	1514	10	AJ006971 Rattus no
18	469	59.4	5345	19	MDAPK
19	445	56.4	1590	9	BC003614 Homo sapi
20	443.4	56.2	5910	9	HSDAPK
21	398.2	50.5	4935	6	AR080622 Sequence
22	398.2	50.5	5886	6	AR121934 Sequence
23	319.8	40.5	4918	10	BC021490 Mus muscu
24	244.6	31.0	132817	2	AC034201 Homo sapi
25	244.6	31.0	210617	2	AC034201 Homo sapi
26	239.4	30.3	247196	2	AC073822 Mus muscu
27	222.4	28.2	194028	9	AC021541 Homo sapi
28	208.6	26.4	3983	4	S57131
29	207	26.2	2960	9	AB056801 Macaca fa
30	203.8	25.8	1317	4	S80867
31	202.2	25.6	1415	9	HSWYOLCKI
32	202.2	25.6	3181	9	AB037663 Homo sapi
33	202.2	25.6	5719	9	AF069601 Homo sapi
34	202.2	25.6	5926	6	AX329738 Sequence
35	202.2	25.6	5926	6	AX330278 Sequence
36	202.2	25.6	5926	6	AX333040 Sequence
37	202.2	25.6	5926	6	AX337264 Sequence
38	202.2	25.6	5926	6	HSU48959 Homo sapien
39	197.4	25.0	1366	3	ACWYINCH
40	197.4	25.0	3426	9	HSNICK
41	195.2	24.7	101222	2	AC103501 Rattus no
42	193.6	24.5	480	6	AR119795 Sequence
43	193.6	24.5	480	6	AR126755 Sequence
44	193.6	24.5	480	6	AR128915 Sequence
45	193.6	24.5	480	6	AR130846 Sequence

## ALIGNMENTS

RESULT 1	AF052941	1742 bp	mrna	linear	PRI 20-JAN-2000
LOCUS	AF052941				
DEFINITION	Homo sapiens DAP-kinase related protein 1 mRNA, complete cds.				
ACCESSION	AF052941				
VERSION	AF052941.1	GI:3560542			
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 1742)				
AUTHORS	Imbal,B., Shani,G., Cohen,O., Kissil,J.L. and Kimchi,A.				
TITLE	Death-associated protein kinase-related protein 1, a novel				
JOURNAL	Mol. Cell. Biol. 20 (3), 1044-1054 (2000)				
MEDLINE	20094983				
PUBMED	10629061				
REFERENCE	2 (bases 1 to 1742)				
AUTHORS	Kimchi,A. and Imbal,B.				
TITLE	Direct Submission				
JOURNAL	Submitted (09-MAR-1998) Molecular Genetics, Weizmann Institute of				
	Science, Rehovot 76100, Israel				

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NIP1PHIKLIDFGLAHEIDEGVEERKNIETGFEVAPAEIVNEPUSLEADMSIGVITY  
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923..1021  
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BASE COUNT 441 a 437 c 504 g 360 t  
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Best Local Similarity 99.9%; Pred. No. 1.4e-172;  
Matches 788; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tatgacatcgagagagagctggagagtgccagttgcacatcgtaagaagtgcggagag 60  
DB 98 TATGACATCGAGAGAGACTGGGAGTGCCAGTTGCCATCGTAAGAAGTCCGGAG 157

QY 61 aagagcaggggcttgatgtaacagcaagttcatcaagaagcggcagagccggcgagc 120  
DB 158 AAGAGCAGGGGCTTGATGATGCAAGCCAAATTCAACAGAGCGGAGCGGGAGC 217

QY 121 cggcgcggtgtgagccggagagatcgagcgggagtgtaagatctcgcggcagggtgctg 180  
DB 218 CGGCGGCTGTGAGCCGGAGAGATCGAGCGGAGTGAGACATCCTCGCGCAGGTGCTG 277

QY 181 caccacaatgcatcagctcagcagctctatgagaacccgacccgaagtggtgacatc 240  
DB 278 CACCAATGTCATCACCTGCTCAGACGCTGTATGAAACCCACGACGCTGCTCATC 337

QY 241 cttagagctagtgctgagagagagctctcgatctcctgcccgaagaagtgtaactgagt 300  
DB 338 CTTGAGCTAGTGTCTGGAGGAGAGCTTTTCATTTTCCTGGCCAGAAAGAGTCACTAGT 397

QY 301 gagagagagagccacacagctcatcaagcagatcctgagtggtgtaactaccctcaaca 360  
DB 398 GAGAGAGGAGGCCACACGCTTCATTAAAGCAGATCCTGGATGGGGTGMACTACCTTCACACA 457

QY 361 aagaaaattgctcacttgatctcaagccagaacacatattggtttgagaagaataatt 420  
DB 458 AAGAAAATTGCTCATTGATCTCAAGCCAGAAAACATTATGTTGTTAGACAAGATATT 517

QY 421 cccattccacacatcaagcttgatgtaacttgctgctgcgcacgaataatgagaatgagt 480  
DB 518 CCCATTCCACACATCAAGCTGATTGACTTTGCTGGCTCAAGAAATGGAAGATGAGACTT 577

QY 481 gaatttaagaataatttttgagagcgggaatttgctgctcagaagaattgtaactagag 540  
DB 578 GAAATTTAAGAAATATTTTGGAGCCCGGAATTTGTTGCTCCAGAAATGTGAACATACGAG 637

QY 541 cccctgggtctgagagctgagacatgtagagcagtagcgtcatcacactatactcttaagt 600  
DB 638 CCCCTGGGTCTGAGAGCTGACATGTGAGACATTAAGCGCTCACTACCTTACTTTAAGT 697

QY 601 ggaagcattcccttctctgagagacaggaagcaggaataaacatctgcaaatatcacatcagt 660  
DB 698 GGAGCATCCCTTCTCTGAGAGACAGGAAGCAAGTAACATGGAATAATCATCACTAAGTG 757

QY 661 agttaagacttgatgaggaattcttccagcatacgagcagcgtgccaaggaattatt 720

DB 758 ACTTACGACTTGTGATGAGGAATTTCTCAGCCATACGAGGAGCTGGCCAAAGCACTTATT 817

QY 721 cggagagctctgtttaaagagaccggaaagcgctacaatccaaaggctctcagagac 780  
DB 818 CGGAAGCTTGTGTTAAAGAGACCGGAACGGCTCACAATCCAGAAGGCTCTCAGACAC 877

QY 781 cccctgagatc 789  
DB 878 CCTTGATC 886

RESULT 2  
AB018001 1739 bp mRNA linear pri 04-DEC-1999  
LOCUS AB018001  
DEFINITION cDNA for Death-associated protein kinase 2, complete cds.  
ACCESSION AB018001  
VERSION AB018001.1 GI:6521209  
KEYWORDS Death-associated protein kinase 2.  
SOURCE Homo sapiens CDNA to mRNA.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
Kawai,T., Nomura,F., Hoshino,K., Copeland,N.G., Gilbert,D.J.,  
Jenkins,N.A. and Akira,S.  
Death-associated protein kinase 2 is a new  
calcium/calmodulin-dependent protein kinase that signals apoptosis  
through its catalytic activity  
Oncogene 18 (23), 3471-3480 (1999)  
99303018  
REFERENCE 2 (bases 1 to 1739)  
AUTHORS Akira,S. and Kawai,T.  
TITLE Direct Submission  
JOURNAL Submitted (28-SEP-1998) Shizuo Akira, Hyogo College of Medicine,  
Department of Biochemistry, Mukogawa-cho 1-1, Nishinomiya, Hyogo  
663-8501, Japan (E-mail:akira@hyo-med.ac.jp, Tel:81-798-45-6357,  
Fax:81-798-46-3164)

FEATURES  
source  
Location/Qualifiers  
1..1739  
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31..1143  
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BASE COUNT 439 a 439 c 504 g 357 t  
ORIGIN

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Best Local Similarity 99.6%; Pred. No. 7.6e-172;  
Matches 786; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tatgacatcgagagagagctggagagtgccagttgcacatcgtaagaagtgcggagag 60  
DB 97 TATGACATCGAGAGAGACTGGGAGTGCCAGTTGCCATCGTGAAGAAGTCCGGAGAG 156

QY 61 aagagcaggggcttgatgtaacagcaagttcatcaagaagcggcagagccggcgagc 120

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Db 157 AAGAGACGGGGCTTGATGATGACGCAAGTTCATCAAGAGGGGACAGACGGGGAGC 216
Qy 121 cggcgcggtgtgagccgggagagatcgagcgggaggttgacatccttgccaggtgtc 180
Db 217 CGCGCGGgtgtgagccgggagagatcgagcgggaggttgacatccttgccaggtgtc 276
Qy 181 caccacaatgtcatcagcgtgcagcagcgtctatagagaacggcagcagcgtgtgtgacatc 240
Db 277 CACCAAAATGTCATCAGCTGACGACGCTTATGAGAACCGCACCGAGTGGTGTATC 326
Qy 241 ctgagactagtgcttgagagagagccttcgatcttccttgccagagagagagagagag 300
Db 337 CTGAGACTAGTGTCTGGAGAGAGAGCTCTTGATTCCTGGCCAGAAAGAGTCACTGAGT 396
Qy 301 gagagagagagccacagcagctcatcaagcagatccttgatgaggttgagactcttcaca 360
Db 397 GAGGAGAGAGCCACAGCTTCATTAAAGCAATCTGGATGGGTGAACTACCTTCACACA 456
Qy 361 aagaaatgtcacttgatctcaagccagaaacatratgtttatagacaagaatatt 420
Db 457 AAGAAAATGCTCATTGTTGATCTCAAGCCAGAAACATTATGTTGTAGACAAATATT 516
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Db 517 CCATTCCACACATCAAGCTGATTGACTTGGTCTGGCTCAGCAAAATAGAAATGAGAT 576
Qy 481 gaatttaagaatatttttgagagagcgggaattgtgtctcagaatattgtgaactacag 540
Db 577 GAATTTAAGAAATTTTGTGGAGCGCGGAATTTGTGCTCCAAATTTGAACTACGAG 636
Qy 541 cccctggtcttgagagctgacatgctgagagatagcgatcaacacacacacacacac 600
Db 637 CCCCTGGCTTGAGAGCTGACATGTGAGAGATAGGCGTCACTACCTTACCTTTAAGT 686
Qy 601 gggagcattccctctccttgagagacacgagacgagaaacacacacacacacacacac 660
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Db 877 CCCTGGATC 885

RESULT 3
LOCUS BC022165 1883 bp mRNA linear ROD 28-JAN-2002
DEFINITION Mus musculus, death-associated kinase 2, clone MGC:13742
IMAGE:4016911, mRNA, complete cds.
ACCESSION BC022165
VERSION BC022165.1 GI:18381096
KEYWORDS MGC.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1883)
AUTHORS Strausberg, R.
TITLE Direct Submision
JOURNAL Submitted (25-JAN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.ncl.nih.gov
COMMENT Contact: MGC help desk
```

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Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbio.org
Contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whitting

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov
Series: IRAK Plate: 18 Row: f Column: 7
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 6521216.

FEATURES
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BASE COUNT 576 a 444 c 471 g 392 t
ORIGIN
Query Match 88.4%; Score 697.8; DB 10; Length 1883;
Best Local Similarity 92.8%; Pred. No. 9.2e-152;
Matches 732; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

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Qy 61 aagagcaggggttgatgagcagcaagttcatcaagaagcgagacggcgagc 120
Db 217 AAGAGCACAGGCTGTGAGTATGACAGCCAAAGTTCTTAAAGAGAGCGAGCCGGCCAG 276
Qy 121 cggcgcggtgtgagccgggagagatcgagcgggaggttgacatccttgccaggtgtc 180
Db 277 CGTGGGGCTGTGCGGGAGAAATGACGGAGGTGACATCTTCCGCGAGGTCTG 336
Qy 181 caccacaatgtcatcagcgtgcagcagcgtctatagagaacggcagcagcgtgtgtgacatc 240
Db 337 CACCCCAACATCATACAGCGTCTATGAGAGACCGACCGACGAGTGGTGTATC 396
Qy 241 ctgagactagtgcttgagagagagccttcgatcttccttgccagagagagagagagag 300
Db 397 CTGAGACTAGTGTCTGGAGAGAGAGCTCTTGATTCCTGGCCAGAAAGAGTCACTGAGT 456
Qy 301 gagagagagagccacagcagctcatcaagcagatccttgatgaggttgagactcttcaca 360
Db 457 GAGGAGAGAGCCACAGCTTCATTAAAGCAATCTGGATGGGTGAACTACCTTCACACA 516
Qy 361 aagaaatgtcacttgatctcaagccagaaacatratgtttatagacaagaatatt 420
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LOCUS AF052942 1474 bp mRNA linear ROD 20-JAN-2000  
DEFINITION Mus musculus DAP-kinase related protein 1 mRNA, partial cds.  
ACCESSION AF052942  
VERSION AF052942.1 GI:3560544  
KEYWORDS house mouse,  
SOURCE Mus musculus  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sclurognathu; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 1474)  
AUTHORS Inbal,B., Shani,G., Cohen,O., Kissil,J.L. and Kimchi,A.  
TITLE Death-associated protein kinase-related protein 1, a novel  
serine/threonine kinase involved in apoptosis  
JOURNAL Mol. Cell. Biol. 20 (3), 1044-1054 (2000)  
MEDLINE 20094983  
PUBMED 10629061  
REFERENCE 2 (bases 1 to 1474)  
AUTHORS Kimchi,A. and Inbal,B.  
TITLE Direct Submission  
JOURNAL Submitted (09-MAR-1998) Molecular Genetics, Weizmann Institute of  
Science, Rehovot 76100, Israel  
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source location/Qualifiers  
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/db\_xref="GI:3560545"  
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IDFLAHEIDGVEFKNIGTPEFVAVETVAVPLGLADWMSIGVTVYLLSGASP  
LGDITKOTLANIVADVDFEEFQSTSEAKPIRKLTLREPRKRLTIOEALRHPI  
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Matches 602; Conservative 0; Mismatches 54; Indels 0; Gaps 0;  
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Db 1 GCCGGAGAGAAATCGAGCGGAGGTGAGCATCTGCGGACAGTGCTGCACCCCAACATCA 60  
OY 194 tcagcgcgacgaagctctatgagaaacgcgacagcggtgagacatccttgagctagtgt 253  
Db 61 TCACGAGGACGACGAGCTCATGAGAACCGACGAGTGCTGCTCATCTTACGCTAGTGT 120  
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Db 121 CCGGAGAGAACCTGTTGATTTCTCTGGCCCGAAGAGACTCTTAAAGTAGAGAGAGCCA 180  
OY 314 ccagcctcatatgaacagatcctgagtgaggactcactcacacaagaanaattgctc 373  
Db 181 CCACCTTCATTAAGCAGATCTCGATGGGGTGAATTAACCTTCACACAAGAAATTTGCTC 240  
OY 374 acttgatctcaagccagaaacattatgtctgtagacaagaataatcccatccacaca 433  
Db 241 ACTTTGATCTCAACCCAGAAAACATCATGTTGTAGACAAATAATCCCAATTCACACA 300  
OY 434 tcagcgcgacgtactctgctctcagacagaaatagaaagatgaggttgagtaataa 493  
Db 301 TCAAGCTGATGACTTTGGCTGGCTGCACGAAATAGAAAGATGAGATTGAATTTAAAAACA 360  
OY 494 ttcttggaagcgcggaattgtgctccagaatgtgtaactagagagccctgggtctg 553  
Db 361 TTTTGGACACCTGAATTTGTGCTCCAGAAATCGTAACATATGAGGCACTGGGACTGG 420

RESULT 6  
AB022341 2055 bp mRNA linear PRI 24-JUN-1999  
LOCUS  
DEFINITION Homo sapiens mRNA for ZIP kinase, complete cds.  
ACCESSION AB022341  
VERSION AB022341.1 GI:5162883  
KEYWORDS ZIP kinase.  
SOURCE Homo sapiens cell\_line:Hela RCB0007 CDNA to mRNA, clone\_lib:Hela  
cell CDNA library.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (sites)  
AUTHORS Murata-Hori,M., Suizu,F., Iwasaki,T., Kikuchi,A. and Hosoya,H.  
TITLE ZIP kinase identified as a novel myosin regulatory light chain  
JOURNAL FEMS Lett. 451 (1), 81-84 (1999)  
MEDLINE 99283879  
REFERENCE 2 (bases 1 to 2055)  
AUTHORS Iwasaki,T., Murata-Hori,M. and Hosoya,H.  
TITLE Direct Submission  
JOURNAL Submitted (12-JAN-1999) Takahiro Iwasaki, Hiroshima University,  
Department of Biological Science, 1-3-1 Kagamiyama,  
Higashi-Hiroshima, Hiroshima 739-8526, Japan  
(E-mail:u0775006@ipc.hiroshima-u.ac.jp, Tel:81-824-7443(ex.7443),  
Fax:81-824-0734)  
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source location/Qualifiers  
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QY 601 ggaacatcccttcccttgagagacagaaagcaatggaataatcacatcaatg 660  
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QY 781 cccttgatc 789  
Db 826 TCCTGGATC 834

RESULT 8  
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LOCUS AR076190 1429 bp DNA linear PAT 30-AUG-2000  
DEFINITION Sequence 4 from patent US 5958748.  
ACCESSION AR076190  
VERSION AR076190.1 GI:10002936  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1429)  
AUTHORS Akira,S. and Kawai,T.  
TITLE DNA coding for serine/threonine kinase  
JOURNAL Patent: US 5958748-A 4 28-SEP-1999;  
FEATURES  
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BASE COUNT 309 a 425 c 475 g 220 t  
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Query Match 62.7%; Score 494.6; DB 6; Length 1429;  
Best Local Similarity 76.7%; Pred. No. 1.5e-104;  
Matches 605; Conservative 0; Mismatches 184; Indels 0; Gaps 0;

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QY 121 cggcgagtggtgagccggagagagatcgagcggagagtgagcatccttgcgagtgctg 180  
Db 166 CGCGCGGCTGTGAGCGGAGGAGATCGAAGCGAGGTGAGCATCTGCCCGAGATCCGC 225  
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QY 241 ctgagctagtgctgagagagagcttcgattccttgccagagagagagagagagagag 300  
Db 286 CTGAGACTGGTGTCCGCTGCGAGCTTTTGCAGCTTCTGCGCAGAAAGAGTCAATTGACG 345  
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QY 721 cggaaagcttctgttaagaagaccggaagagctcacaatccaagaagcttcagaac 780  
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RESULT 9  
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LOCUS AR124103 1429 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 4 from patent US 6171841.  
ACCESSION AR124103  
VERSION AR124103.1 GI:14109464  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1429)  
AUTHORS Akira,S. and Kawai,T.  
TITLE DNA coding for serine/threonine kinase  
JOURNAL Patent: US 6171841-A 4 09-JAN-2001;  
FEATURES  
source 1..1429  
BASE COUNT 309 a 425 c 475 g 220 t  
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Query Match 62.7%; Score 494.6; DB 6; Length 1429;  
Best Local Similarity 76.7%; Pred. No. 1.5e-104;  
Matches 605; Conservative 0; Mismatches 184; Indels 0; Gaps 0;

QY 1 tatgacatcggagagagctgggagtgagcttgccatcgctgaagaagtgcggag 60  
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QY 121 cggcgagtggtgagccggagagagatcgagcggagagtgagcatccttgcgagtgctg 180  
Db 166 CGCGCGGCTGTGAGCGGAGGAGATCGAAGCGAGGTGAGCATCTGCCCGAGATCCGC 225  
QY 181 caccacaatgtcatcagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 240  
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RESULT	10			
LOCUS	E23385			
DEFINITION	E23385	1429 bp	DNA	linear
ACCESSION	E23385			
VERSION	E23385.1			
KEYWORDS	JP 1999098984-A/2.			
SOURCE	unidentified.			
ORGANISM	unidentified			
REFERENCE	1 (bases 1 to 1429)			
AUTHORS	Shizuo, S.T.K.K.			
TITLE	DNA encoding serine/threonine kinase			
JOURNAL	Patent: JP 1999098984-A 2 13-APR-1999;			
COMMENT	SCIENCE & TECH AGENCY			
OS	Unidentified			
PN	JP 1999098984-A/2			
PD	13-APR-1999			
PF	26-SEP-1997 JP 1997261589			
PR				
PI	SHIZUO SHINRA, TARO KAWAI			
PC	C12N15/09, C12N1/21, C12N9/12// (C12N15/09, C12R1:91), (C12N1/21,			
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QY	61	aagagcaacggggtcttgagatctgcagccaaqtlcatcaagaagggcgagacggcgagc	120
Db	106	AAGGCAAGCGGGCATGGAGTMTGCGCCAAATTCATCAAGAGGGCGCTGCATCCAGC	165
QY	121	cggcgcggtgtgagccgggagagagatcggacgggaggttgagcactctgtggcgaggtgcg	180
Db	166	CGGCGCGGTGTGAGCCGGGAGAGATGAAACGGGAGGTGAGCTTCCTGCGCGAGATCCGC	225
QY	181	caccacaaatgcatcaagcgtgcacgacgtctatagaagaccgacgcagctggtgcacatc	240
Db	226	CACCCCAACATCATACACTGCACTGACGTGTGGAGAACAAAGACAGTGGTGCTGATC	285
QY	241	cttgagctagtgctcgbgagagagccttcgatctccctggccagaagagatcactgagt	300
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QY	301	ggagggagggcgcaacagcttaataagaagatccctgtgatgggtgaaactacctcaaca	360
Db	346	GAGGATGAGGGCCAGCACTTCTTAACAANAATCTTAGACGTGTCCACTTCCTGCACCTGC	405
QY	361	aagaaatctgcacttgcacttgcatacgaacgaanaacatlaytltgtagaagaaatatt	420
Db	406	AAGGCATGTGCACTTGAGCTGAAGCGCCGAGAACATCATGTTGGTGGCAAGCACGCA	465
QY	421	cccatccacacataagactgatatgacttgtgtcgtctcaagaaatagaagttgaatt	480
Db	466	GCCAGCCCCCGATTATACCTCATGACTTTGGCATCGCGCACAGATCGAGCTGGCAGC	525
QY	481	gaattaaagaatatttttggagcgccggaatttgtctccagaatattgaaactacgag	540
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QY	661	agtaagacttgcataggaatctcttcagacatacgaacgagctgtgcgaagacttaatt	720
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QY	721	cggaaagctctcgttaagaagaccccgaaacggctcaacatccaagggctcttaagcac	780
Db	766	CGAGAGCTGCTGTGTAAGAAGACCCCAAGAGAGGAGATGACCATGCGACAGAGCTGTGACAT	825
QY	781	ccctgagatc 789	
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RESULT	11			PRI 25-FEB-1998
LOCUS	AB007144			
DEFINITION	AB007144	2105 bp	mRNA	linear
ACCESSION	AB007144			complete cds.
VERSION	AB007144.1	GI:2911155		
KEYWORDS	ZIP-Kinase.			
SOURCE	Homo sapiens cDNA to mRNA.			



ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 2105)  
AUTHORS Akira, S. and Kawai, T.  
TITLE Direct Substitution  
JOURNAL Submitted (10-SEP-1997) Shizuoka Akira, Hyogo College of Medicine,  
Department of Biochemistry, Mukogawa-cho 1-1, Nishinomiya, Hyogo  
663, Japan (E-mail: akira@hyo-med.ac.jp, Tel: +81-798-45-6357,  
Fax: +81-798-46-3164)  
2 (sites)  
REFERENCE Kawai, T., Matsumoto, M., Takeda, K., Sanjo, H. and Akira, S.  
AUTHORS ZIP kinase, a novel serine/threonine kinase which mediates  
TITLE apoptosis  
JOURNAL Mol. Cell. Biol. 18 (3), 1642-1651 (1998)  
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DB 250 CGCGGTGGGTGAGCGGCGAGGAGATCGACGGAGAGGTGAACATCTCGCGGAGATCCGG 309  
QY 181 caccacaatgtcatcagcgtcgacagagctctatagagaacgcagcagcgtgtgtgacatc 240  
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QY 241 cttagagctagtgctgagagagagccttcgattcccttgaccagagagagtgactagat 300  
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QY 301 gaggagagcgacacagcgtctatcaagcagatccctgagtgagggtgaactacatcacaca 360  
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DB 490 AACGGCATTCACACTTTTGACCTGAAGCCGGAACATCATCTGCTGGAGCAAGAACGTG 549  
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DB 610 GAGTTCAAGAAACATCTTCGGCACCCCGAGATTGTGGCCCCAGAGATTGGAAGTATGAG 669  
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DB 910 TCCTGGAT 917  
RESULT 12  
AR076189 AR076189 2132 bp DNA linear PAT 30-AUG-2000  
LOCUS Sequence 3 from patent US 5958748.  
DEFINITION AR076189  
ACCESSION AR076189  
VERSION AR076189.1 GI:10002935  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2132)  
AUTHORS Akira, S. and Kawai, T.  
TITLE DNA coding for serine/threonine kinase  
JOURNAL Patent: US 5958748-A 3 28-SEP-1999;  
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source Location/Qualifiers  
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Query Match 62.6%; Score 493.6; DB 6; Length 2132;  
Best Local Similarity 76.6%; Pred. No. 2.7e-104;  
Matches 604; Conservative 0; Mismatches 184; Indels 0; Gaps 0;  
QY 1 tatgaatcggaaagagagcggtgagtgccattgcccctgctgaagaagtcggagag 60  
DB 130 TATGAATGGGGGAGGAGCTGGCGACGGCCACTTTCGTCGCGAAGTGC CGGAC 189  
QY 61 aagagacaggggcttgagtaatgcagcaagttcatcaagaagcgagcgaggagc 120  
DB 190 AAGGACGCGGCGAAGGAGTACGACCAAGTTCATCAAGAAGCGCCCGCTGTATCCAGC 249  
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DB 250 CGCGGTGGGTGAGCGGCGAGGAGATCGACGGAGAGGTGAACATCTCGCGGAGATCCGG 309  
QY 181 caccacaatgtcatcagcgtcgacagagctctatagagaacgcagcagcgtgtgtgacatc 240  
DB 310 CACCCCAACATCATCAACCCCTCGACGACATCTTGAGAAAGACGAGCTGGTCTCATC 369  
QY 241 cttagagctagtgctgagagagagccttcgattcccttgaccagagagagtgactagat 300  
DB 370 CTGAGACTGTCTCTGGCGGGAGCTTTTGACTTCTCTGGCGAAGAAAGTGGCTGACG 429

QY	181	caccacaatgtcatcaacgctgcacgaagcttatatgaagaccgcgaacgctgtgtgacacatc	240
Db	310	CACCCCAACATCATCACCTCGACAGACATCTTGAGAACAAAGACGGACGGCGTCTCATC	369
QY	241	cttgaagctagtgtcttgaagagagctcttcgatcttccttgccccagaagagctaacgagc	300
Db	370	CTGAGAGTGGTCTCTGGCGGGAGAGCTTTTGACTCTCTGGCGGAGAAAGAGTGGCTGACG	429
QY	301	gaggagagagccacacgaagcttcattaaagacaagatccctgtgaatggggtgaactaccctcacaca	360
Db	430	GAGAGACGAGGCGACACCGAGTTCCTCAAGACAGATCCTGGACGGCGTTCACTACCTCGACTCT	489
QY	361	aagaanaattgtcgaactcttgatcttcaagcccgaaanaacatctatgtgttgaagacaagaatattc	420
Db	490	AAGGGCATTCGGACACTTTGACTTGAACCCGGAAACATCATGCTGCTGGACAAAGAACGTCG	549
QY	421	cccatccacacacacaaagctgatctgaacttgtcttgctcgaagaaatagaagatlgaggtc	480
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QY	481	gaatttaagaatatttttggagagccgggaatttgtctccagaanaatttgaactaagag	540
Db	610	GAGTTCAGAACATCTTGCGGACCCCGGAGATTGTGGCCCGACAGATTGTGAACTTATGAG	669
QY	541	ccccgggtcttggagagctgcagatcttgagagaaatggagacgtcacacactacatctcttaag	600
Db	670	CCGCTGGGCTGGAGACCGGACATGTGGAGCATTCGTGTCATCACCTATATCTCTCGTAGC	729
QY	601	ggagacatcccttctctcttggagacacagaagagaacactgtgcaaatatacatctcgtg	660
Db	730	GGTGCATCCCGCTTCTCTGGCGAGACCAAGAGAGAGCGCTCACCCAMCATCTTGACGCGTG	789
QY	661	agttacgaatttgaatgaagaaattcttgaagcaataagcgaagctgtgccaagaagacttaatt	720
Db	790	AACATCGACTTTCAGAGAGAGTACTTTCAGCAACACGACGAGCTGCCAAGAGCTTCATT	849
QY	721	cggaaagctcttcttgaagagaccccggaagacggtcacaatccaaagagctctcagaacac	780
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RESULT 14			
LOCUS	E23384	2132 bp	DNA
DEFINITION	DNA encoding serine/threonine kinase.		
ACCESSION	E23384		
VERSION	E23384.1	GI:13024386	
KEYWORDS	JP 199098984-A/1.		
SOURCE	unidentified.		
ORGANISM	unclassified.		
REFERENCE	1 (bases 1 to 2132)		
AUTHORS	Shizuo,S.T.K.K.		
TITLE	DNA encoding serine/threonine kinase		
JOURNAL	Patent: JP 199098984-A 1 13-APR-1999.		
COMMENT	SCIENCE & TECH AGENCY		
	OS Unidentified		
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	PD 13-APR-1999		
	PF 26-SEP-1997 JP 1997261589		
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	PC C12N15/09,C12N1/21,C12N9/12//C12N15/09,C12R1.91),(C12N1/21,		
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Query Match		62.6%; Score 493.6; DB 6; Length 2132;		
Best Local Similarity		76.6%; Pred. No. 2.7e-104;		
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DB	190	AAGGACCGGGCAAGGAGTACGCCAAGTTCATCAAGAAAGCGCCGCTGTATCCAGC	249	
OY	121	cgagcgagtgtagcccgagagagatcagcgagggtgagcatcctcgcgagtgctg	180	
DB	250	CGCGGTGGGGTGAAGCCGGAGAGATCGAGCGGAGGTGAACATCTCGGGAGATCCG	309	
OY	181	caccacaatgtcaacagctcagcagagctatgaagaaccgacagcgagtggtgacatc	240	
DB	310	CACCCCAACATCATCACTCGACAGACATCTTGAGAACAAAGAGAGCTGTCTCATC	369	
OY	241	cttgagctagtgcttgagagagagctctcgaattccttgccagaaagagtagt	300	
DB	370	CTGAGAGTGTCTCTGGCGGGAGCTCTTGACTTCTGTGGGGAAGAAGTGGCTGACG	429	
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DB	550	CCCAACCCAGAAATCAAGCTCATCGACTTGGCATCGCGCAAAAGATGAGGGGGGAC	609	
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DB	670	CCGCTGGGCTTGAAGGGGAGCATGTGAGCATGGGTCTCATCACTATATCTCTCAGAC	729	
OY	601	gagagacatcccttctcgtgagagacagaaagaaacacttggaataatcacacatcag	660	
DB	730	GGTGCATCCCGTTCGCGGGAGACCAAGCAAGAGACGCTCAACAACTCTCAGCGTG	789	
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LOCUS				

DEFINITION		Novel genes encoding protein kinase or protein phosphatase.			
ACCESSION		BD004888			
VERSION		BD004888.1 GI:18632849			
KEYWORDS		JP 03074934-T/6.			
SOURCE		Homo sapiens.			
ORGANISM		Homo sapiens			
REFERENCE		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
AUTHORS		1 (bases 1 to 2224)			
TITLE		Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Makamatsu,A., Nagai,K., Otsuki,T., Funahashi,S., Seno,C. and Nezu,J.			
JOURNAL		Novel genes encoding protein kinase or protein phosphatase			
COMMENT		Patent: JP 03074934-T 6 30-JAN-2001;			
		HELI RESEARCH INSTITUTE, TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU SAITO, JUNICHI YAMAMOTO, SHIZUKO ISHII, OMOTASU SUGIYAMA, AI WAKAMATSU, KEIICHI NAGAI, TETSUJI OTSUKI, SHINICHI FUNAHASHI, HIARI SENO, JUNICHI NEZU			
		FJNASHASHI, HIARI SENO, JUNICHI NEZU			
		OS HOMO SAPIENS (human)			
		PM JP 03074934-T/6			
		PD 30-JAN-2001			
		PR 28-JUL-2000 JP 2000005060			
		PR 29-JUL-1999 JP 99P 248036,11-JAN-2000 JP 00P 118776 PR			
		02-MAY-2000 JP 00P 183767,18-OCT-1999 US 60/159590 PR			
		17-FEB-2000 US 60/183322			
		PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, PI			
		KAORU SAITO,			
		PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,			
		PI KEIICHI NAGAI, TETSUJI OTSUKI, SHINICHI FUNAHASHI, CHIARI SENO,			
		PI JUNICHI NEZU			
		PC C12N15/54, C12N15/55, C12N9/12, C12N9/16, C12N5/10, C12N1/21, PC			
		C12N1/19, C07K16/40,			
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DB	311	AAGGCGACGGGCAAGGAGTACGACCAAGTTCATCAAGAAAGCGCCGCTGTATCCAGC	370		
OY	121	cgagcgagtgtagccggagagatcgaagcgagggttgagcatcctcgcgagtgctg	180		
DB	371	CGGCGTGGGGTGAAGCCGGGAGAGATCGAGGGGAGGTGAACATCTTCGCGGAGATCCG	430		
OY	181	caccacaatgtcaacagctcagcagagctatgaagaaccgacagcgagtgtagacatc	240		
DB	431	CACCCCAACATCATCACTCGACAGACATCTTCAGAACAAAGAGAGAGCTGTCTCATC	490		
OY	241	cttgagctagtgcttgagagagagctctcgaattccttgccagaaagagtagt	300		
DB	491	CTGAGAGTGTCTCTGGCGGGAGCTCTTGTACTTCTGTGGGGAAGAGAGTGGCTGACG	550		
OY	301	gagagagagcgacacagctcattgaagagatccctggaatgggtgaaactcctcaca	360		
DB	551	GAGAGCAGGCGCAACCGAGTTCCTCAAGACAGATCTTGAGCGCGTTCACCTCACTCT	610		
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